Enriching target populations for genomic analyses using HCR-FISH

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Abstract

When scientists want to understand microbial populations, they turn to metagenomics. The standard technique, shotgun metagenomics, produces nearly complete genomes, enabling researchers to predict traits within a species. Unfortunately, this method applies to broad populations, making it difficult to precisely link metabolic traits to individual species. Sequencing single cells addresses this shortcoming, but the information provided is often incomplete. Now, researchers have developed a way to target smaller populations for metagenomic sequencing. Before sequencing, the researchers added a critical sorting step using hybridization chain reaction fluorescence in-situ hybridization (HCR-FISH). Isolating a population of interest before the sorted cells were used for shotgun sequencing. The result was a more complete genome of a targeted species with low diversity. The technique provided the team enough precision to analyze metabolic features of bacteria sparsely found feeding on decaying diatom algae. The findings suggest that HCR-FISH may be ideal for high-diversity ecosystems, where standard metagenomic techniques don't work for low-abundance organisms due to noise from more common species, making the analysis of uncharacterized microbes simpler and more accessible.